FIG. 1A

```
                11          20          29          38          47          56
5'  GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

                65          74          83          92          101         110
    ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
                    M   E   S   R   K   D   I   T   N   Q   E   E   L   W   K

                119         128         137         146         155         164
    ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    M   K   P   R   R   N   L   E   E   D   D   Y   L   H   K   D   T   G

                173         182         191         200         209         218
    GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    E   T   S   M   L   K   R   P   V   L   L   H   L   H   Q   T   A   H

                227         236         245         254         263         272
    GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    A   D   E   F   D   C   P   S   E   L   Q   H   T   Q   E   L   F   P

                281         290         299         308         317         326
    CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Q   W   H   L   P   I   K   I   A   A   I   I   A   S   L   T   F   L

                335         344         353         362         371         380
    TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Y   T   L   L   R   E   V   I   H   P   L   A   T   S   H   Q   Q   Y

                389         398         407         416         425         434
    TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    F   Y   K   I   P   I   L   V   I   N   K   V   L   P   M   V   S   I

                443         452         461         470         479         488
    ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    T   L   L   A   L   V   Y   L   P   G   V   I   A   A   I   V   Q   L

                497         506         515         524         533         542
    CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    H   N   G   T   K   Y   K   K   F   P   H   W   L   D   K   W   M   L

                551         560         569         578         587         596
    ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    T   R   K   Q   F   G   L   L   S   F   F   F   A   V   L   H   A   I

                605         614         623         632         641         650
    TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Y   S   L   S   Y   P   M   R   R   S   Y   R   Y   K   L   L   N   W
```

```
          659                 668                 677                 686                 695                 704
GCA TAT CAA CAG GTC CAA CAA AAT AAA GAA GAT GCC TGG ATT GAG CAT GAT GTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   Y   Q   Q   V   Q   Q   N   K   E   D   A   W   I   E   H   D   V

          713                 722                 731                 740                 749                 758
TGG AGA ATG GAG ATT TAT GTG TCT CTG GGA ATT GTG GGA TTG GCA ATA CTG GCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   R   M   E   I   Y   V   S   L   G   I   V   G   L   A   I   L   A

          767                 776                 785                 794                 803                 812
CTG TTG GCT GTG ACA TCT ATT CCA TCT GTG AGT GAC TCT TTG ACA TGG AGA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   L   A   V   T   S   I   P   S   V   S   D   S   L   T   W   R   E

          821                 830                 839                 848                 857                 866
TTT CAC TAT ATT CAG AGC AAG CTA GGA ATT GTT TCC CTT CTA CTG GGC ACA ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   H   Y   I   Q   S   K   L   G   I   V   S   L   L   L   G   T   I

          875                 884                 893                 902                 911                 920
CAC GCA TTG ATT TTT GCC TGG AAT AAG TGG ATA GAT ATA AAA CAA TTT GTA TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   A   L   I   F   A   W   N   K   W   I   D   I   K   Q   F   V   W

          929                 938                 947                 956                 965                 974
TAT ACA CCT CCA ACT TTT ATG ATA GCT GTT TTC CTT CCA ATT GTT GTC CTG ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   T   P   P   T   F   M   I   A   V   F   L   P   I   V   V   L   I

          983                 992                1001                1010                1019                1028
TTT AAA AGC ATA CTA TTC CTG CCA TGC TTG AGG AAG AAG ATA CTG AAG ATT AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   K   S   I   L   F   L   P   C   L   R   K   K   I   L   K   I   R

         1037                1046                1055                1064                1073                1082
CAT GGT TGG GAA GAC GTC ACC AAA ATT AAC AAA ACT GAG ATA TGT TCC CAG TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   G   W   E   D   V   T   K   I   N   K   T   E   I   C   S   Q   L

         1091                1100                1109                1118                1127                1136
TAG AAT TAC TGT TTA CAC ACA TTT TTG TTC AAT ATT GAT ATA TTT TAT CAC CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 *   N   Y   C   L   H   T   F   L   F   N   I   D   I   F   Y   H   Q

         1145                1154                1163                1172                1181                1190
CAT TTC AAG TTT GTA TTT GTT AAT AAA ATG ATT ATT CAA GGA AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   F   K   F   V   F   V   N   K   M   I   I   Q   G   K   K   K   K

AAA AA 3'
--- --
 K
```

FIG. 1B

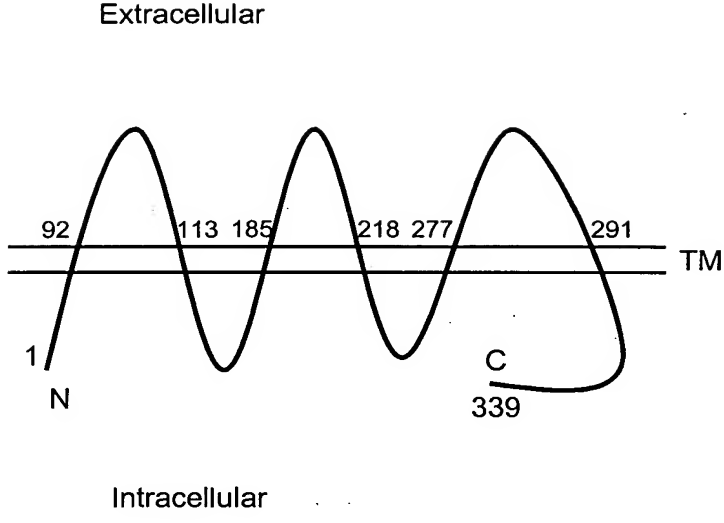
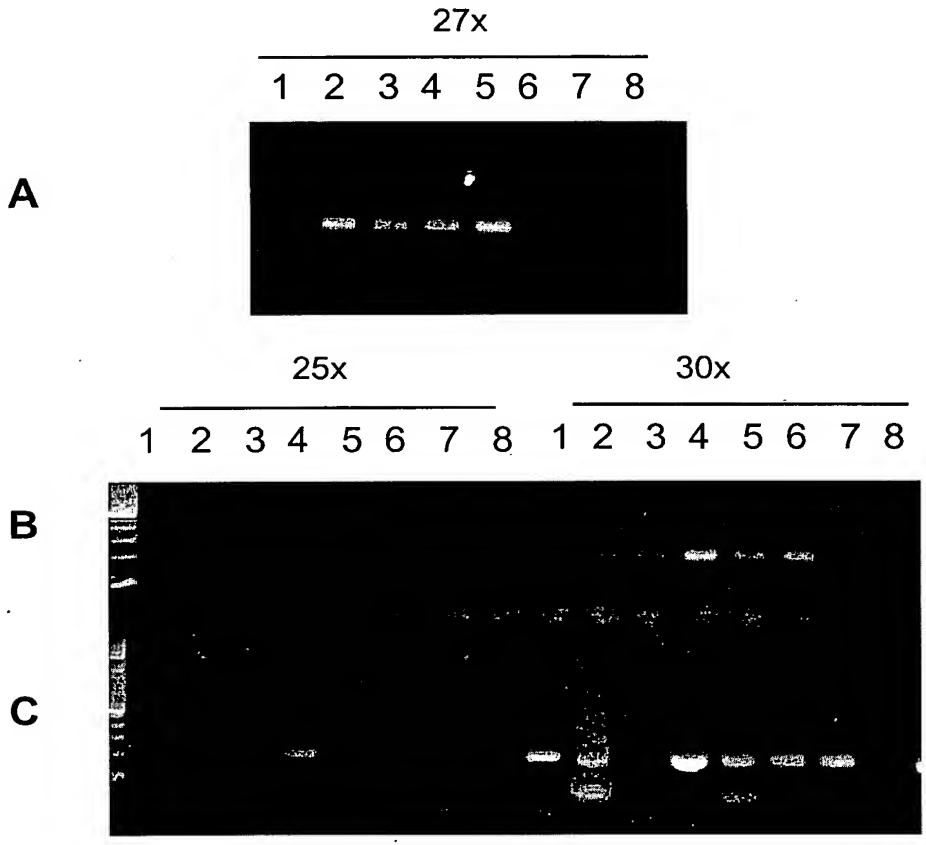


FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3'

FIG. 2



Panels:

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A

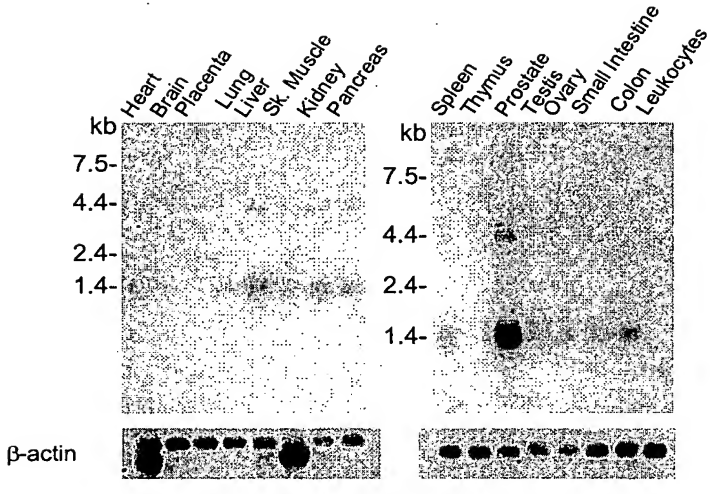
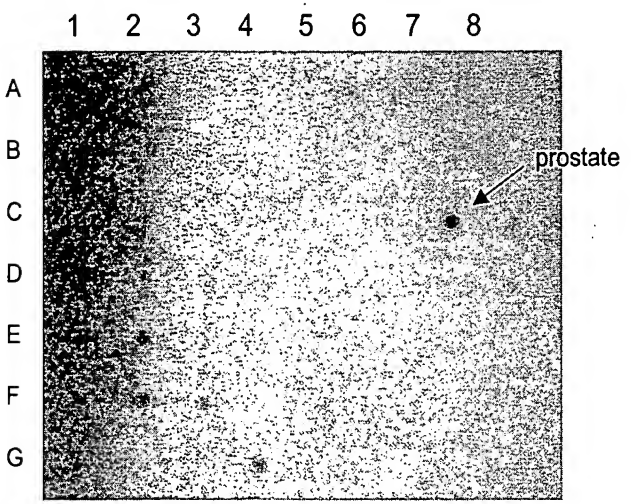


FIG. 3B



A1 brain
A2 amygdala
A3 caudate nucleus
A4 cerebellum
A5 cerebral cortex
A6 frontal lobe
A7 hippocampus
A8 medulla oblongata

B1 occipital lobe
B2 putamen
B3 substantia nigra
B4 temporal lobe
B5 thalamus
B6 sub-thalamic nucleus
B7 spinal cord

C1 heart
C2 aorta
C3 skeletal muscle
C4 colon
C5 bladder
C6 uterus
C7 prostate
C8 stomach

D1 testis
D2 ovary
D3 pancreas
D4 pituitary gland
D5 adrenal gland
D6 thyroid gland
D7 salivary gland
D8 mammary gland

E1 kidney
E2 liver
E3 small intestine
E4 spleen
E5 thymus
E6 peripheral leukocytes
E7 lymph node
E8 bone marrow

F1 appendix
F2 lung
F3 trachea
F4 placenta

G1 fetal brain
G2 fetal heart
G3 fetal kidney
G4 fetal liver
G5 fetal spleen
G6 fetal thymus
G7 fetal lung

FIG. 4

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC

ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG

AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC

ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACA

GTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT

CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG

TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAA

GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT

GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT

ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT

GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG

AGAGAATTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT

ATAGAATATGTTGACTTTACCCCATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT

AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAATAAAAGGCAT

TAAAATATTCTTTGTTTTTTTTTTTTTGTTTGTTTGTTTTTTGTTTGTTTGTTTGTTTTTTTGAGATGAAGTCTCG

CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTC

TCTTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTAGTA

GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC

AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATTT

GCTACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACC

TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGAAA

TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT

ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT

GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAA

TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT

CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGC

CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAG

CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA

TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACA

ATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTTCAACT

AGTAACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA

ACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT

GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT

TGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA

ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTCATATTATTTCCATGTTATC

AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAATCA

CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT

TTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT

GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAG

GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG

TTCACTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG

TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG

ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTTCTTTTGCAGAGCAAGCTAGGA

ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG

TATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATT

CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAG

ATATGTTCCCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCA

AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA

FIG. 5

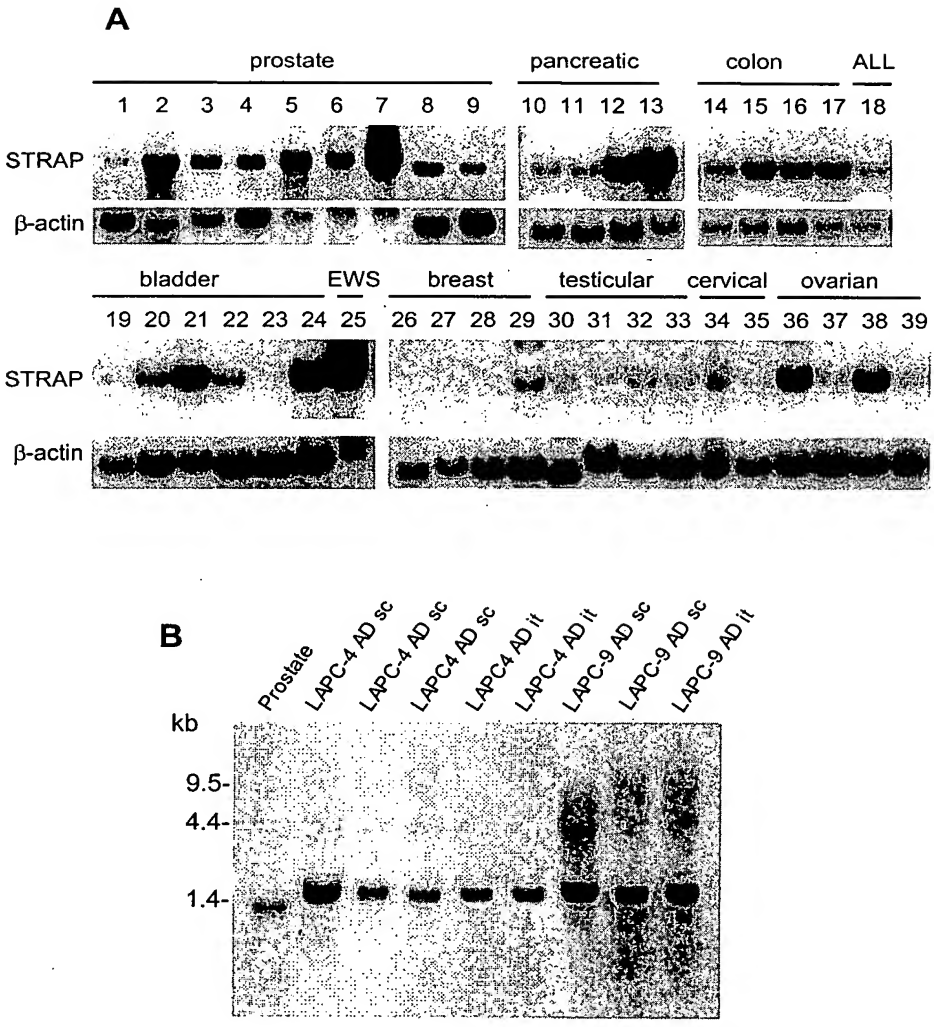


FIG. 6

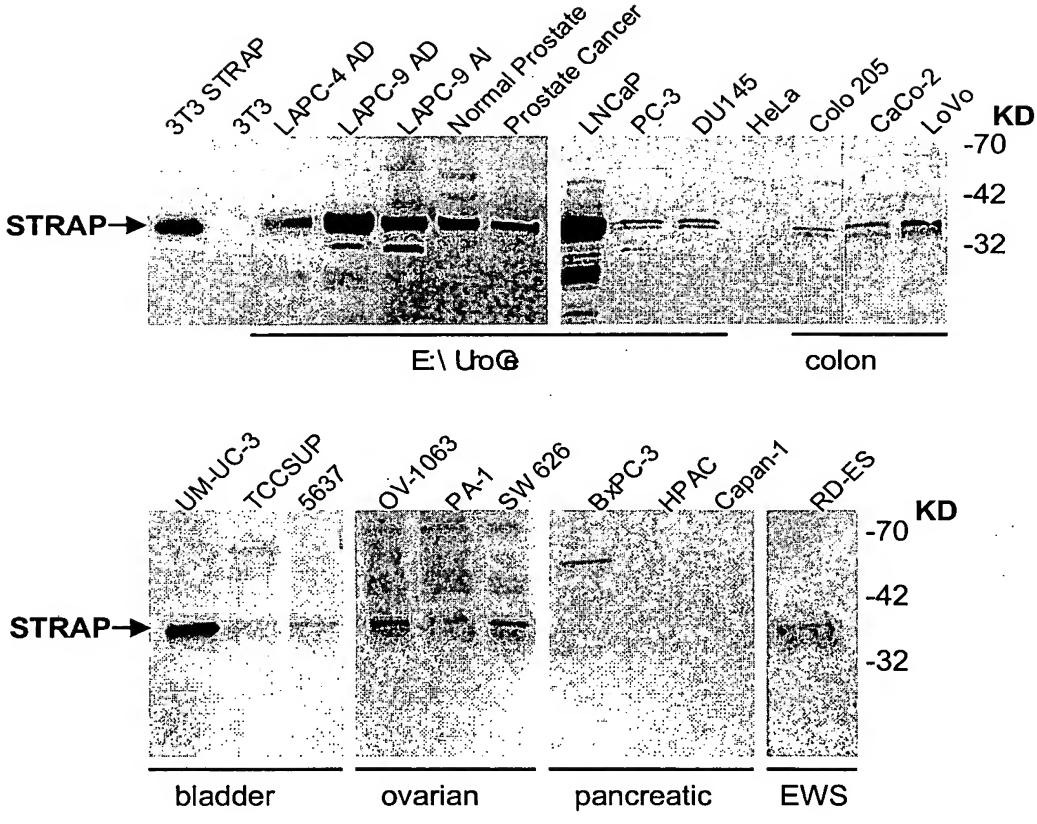


FIG. 7

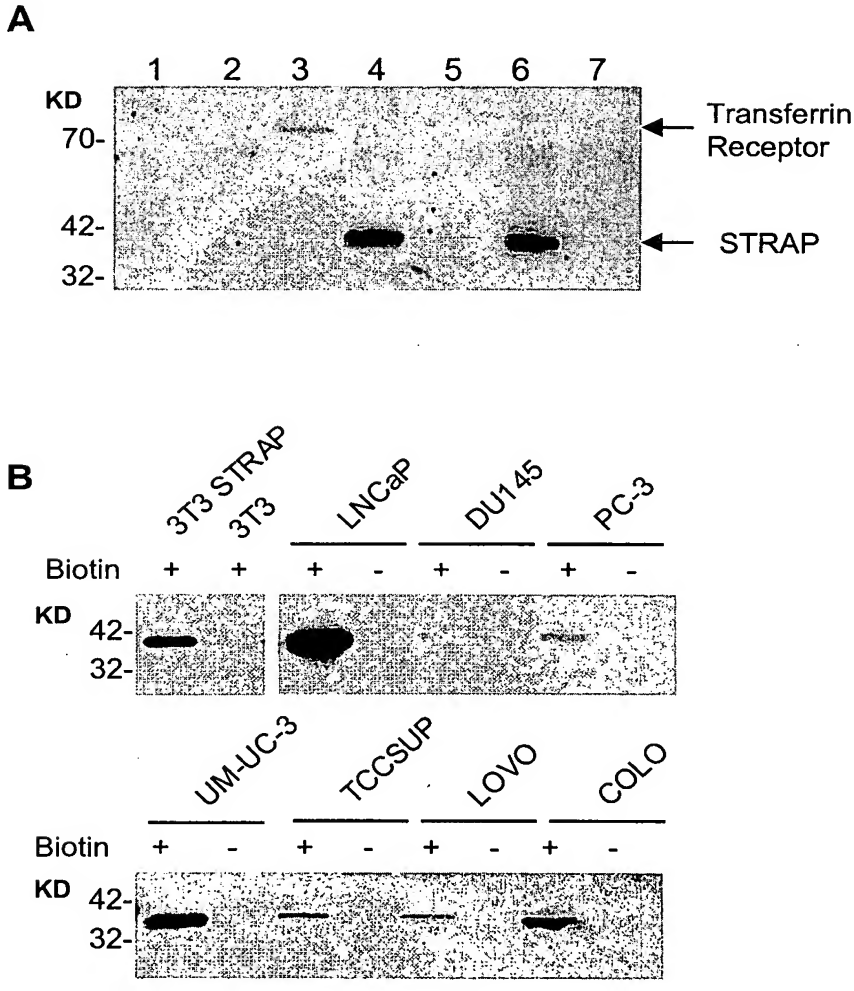


FIG. 8

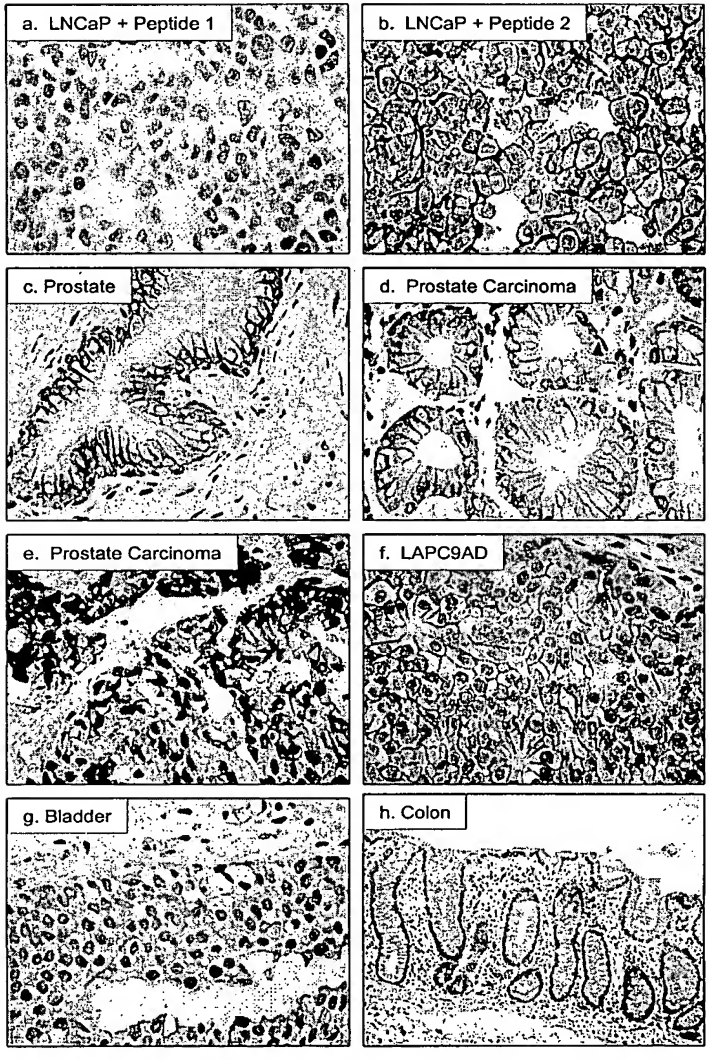


FIG. 9

```
                10          19          28          37          46          55
5'  GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala

                64          73          82          91          100         109
    ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln

                118         127         136         145         154         163
    CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu

                172         181         190         199         208         217
    CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG GTC CAT GTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val

                226         235         244         253         262         271
    GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn

                280         289         298         307         316         325
    ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu

                334         343         352         361         370         379
    GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu

                388         397         406         415         424         433
    TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg

                442         451         460         469         478         487
    GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr

                496         505         514
    TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3'
    --- --- --- --- --- --- --- --- --- --- ---
    Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala
```

FIG. 10

STRAP-2, AA508880 (NCI_CGAP Pr6)
ggtcgacttttccttattcctttgtcagagatctgattcatccatatgctagaaaccaacagagtgacttttaca
aaattcctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctagtataccttgcagg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttggttggaaacctggtta
cagtgtagaaaacagcttggattactaagttgtttcttcgctatggtccatgttgcctacagcctctgcttaccga
tgagaaggtcagagagat

STRAP-2, 98P4B6 SSH fragment
TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAACTGGAATTTGTCTTCCTATTGACTCTACTTCTTTAAAAGCG
GCTGCCCATTACATTCCTCAGCTGTCCTTGCAGTTAGGTGTACATGTGACTGAGTGTTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT

AI139607 (testis EST)
aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaatacttgggtttt
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcaactggagagagttccgatttgt
ccagtccaaactgggttatttgaccctgatcttgtgtacagcccacaccctggtgtacggtgggaagagattcctc
agcccttcaaatctcagatggtatcttcctgcagcctacgtgttagggcttatcattccttgcactgtgctggtga
tcaagtttgtcctaatcatgccatgtgtagacaacacccttacaaggatccgccagggctgggaaaggaactcaaa
acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaaaaa

R80991 (placental EST)
ggccgcggcanccgctacgacctggtcaacctggcagtcaagcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggatggagatctacctctccctgggagtgctggccctcggcacgttgtccctgctggccg
tgacctcactgccgtccattgcaaactcgctcaactggagggagttcagcttcgttcagtcctcactgggctttgt
ggccntcgtgctgagcacactncacacgctcacctacggctggacccgcgccttcgaggagagccgctacaagttc
tacctnccteccaccttcacgntcacgctgctggtgccctgcgttcgttcatcctgggccaaagccctgtttntac
tgccttgcattcagccgnaga

FIG. 11A

```
STRAP-1     106 FYKIPILVINKVLPMVSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFG
STRAP-2       2 FYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLG
                ******   ** ** * **** **** *  **  **  ****  ** **  *   *** *

STRAP-1     166 LLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIV
STRAP-2      62 LLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIM
                *******  *  ***  ***** **  ** *****  * *  * *  *** * * * **

STRAP-1     226 GLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNK
STRAP-2     122 SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
                 *  * ************  * ****  *** ** * **  * * **  *
```

FIG. 11B

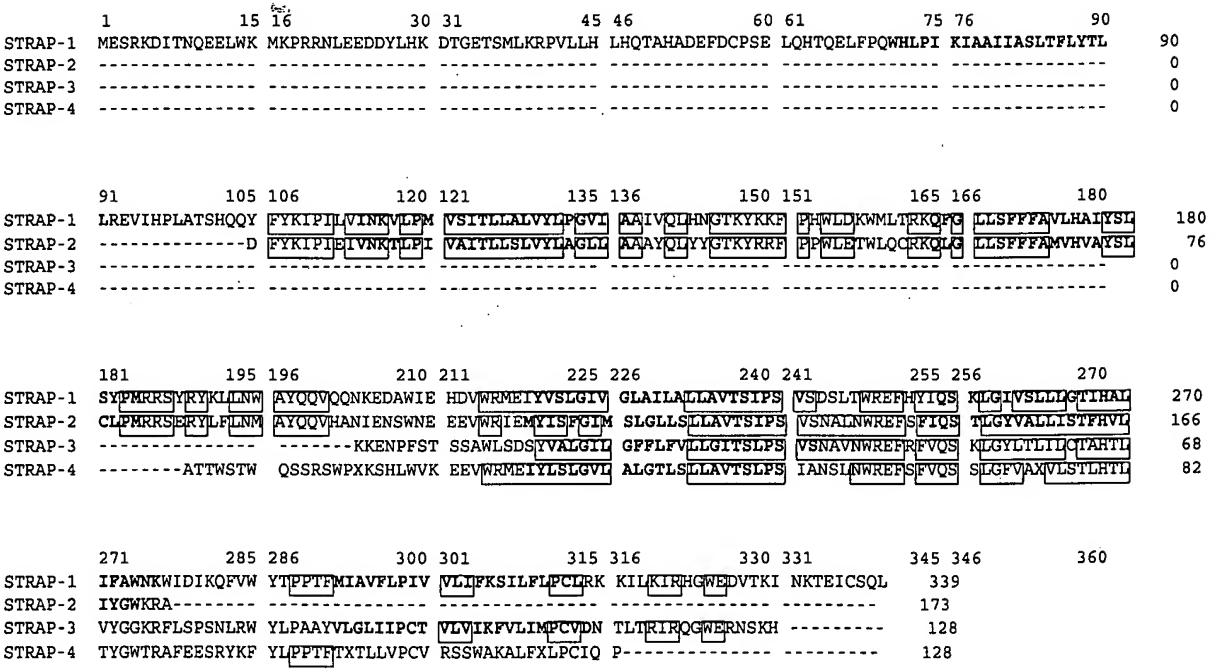
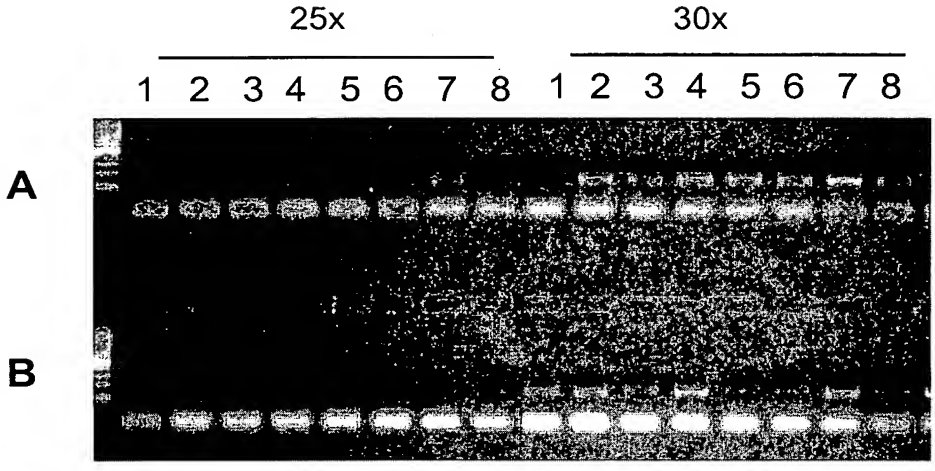


FIG. 12



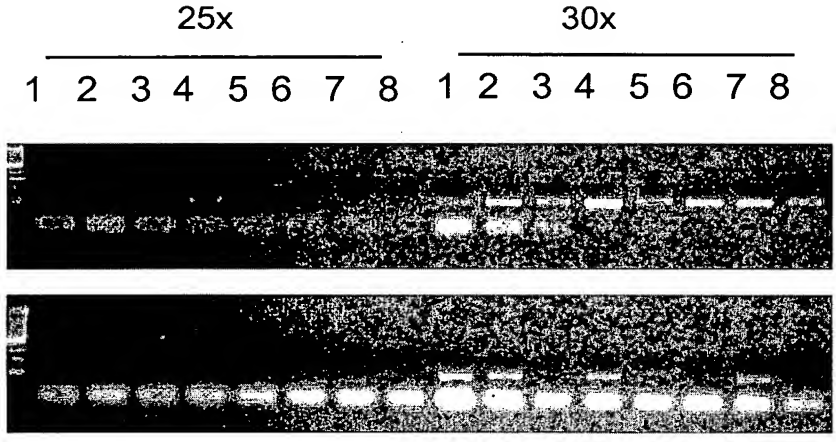
A

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

B

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

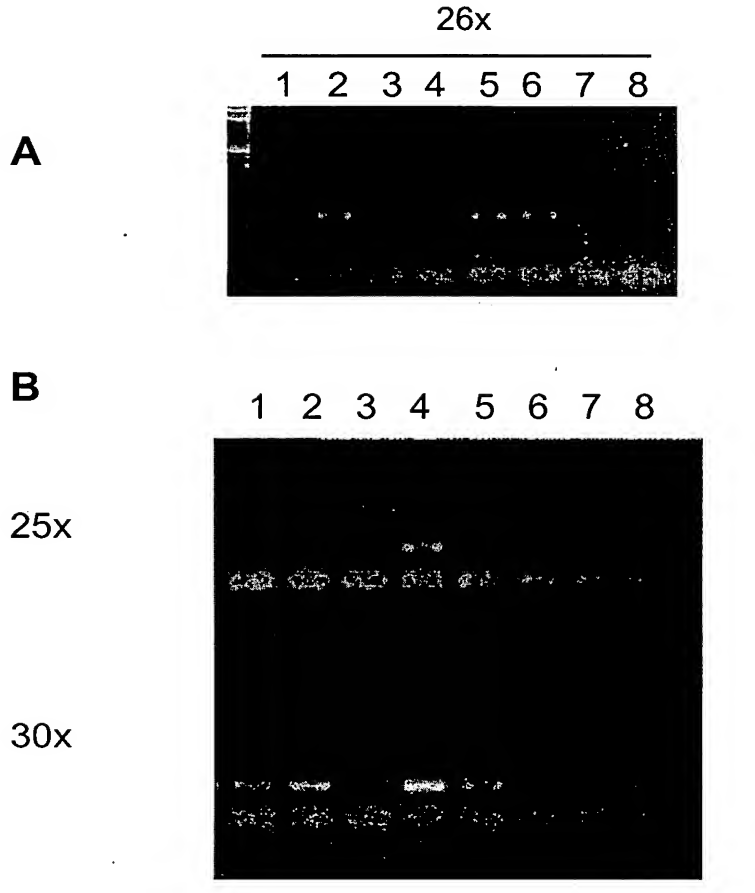
FIG. 13



A
1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

B
1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG.14



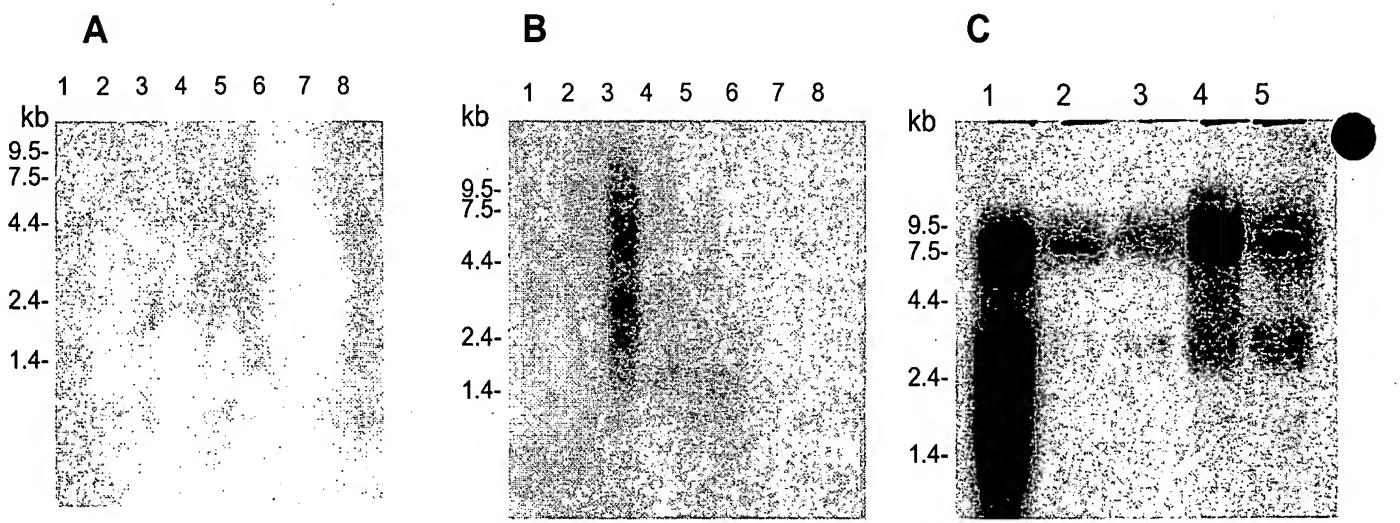
A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 15

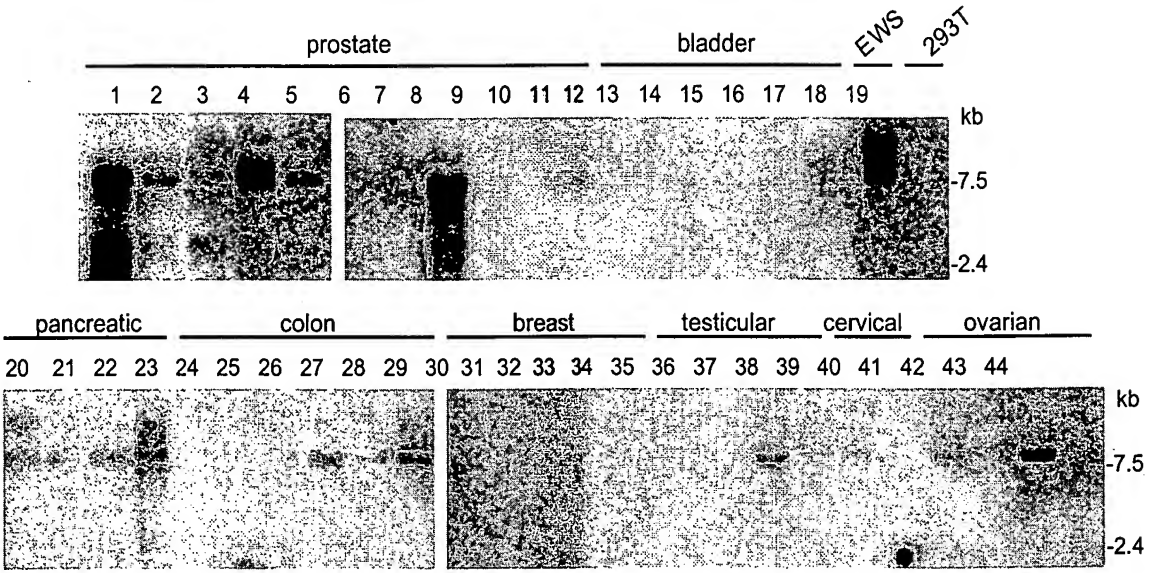


A
1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas

B
1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

C
1. Prostate
2. LAPC-4 AD
3. LAPC-4 AI
4. LAPC-9 AD
5. LAPC-9 AI

FIG. 16



1. prostate
2. LAPC-4 AD
3. LAPC-4 AI
4. LAPC-9 AD
5. LAPC-9 AI
6. TsuPr1
7. DU145
8. LNCaP
9. PC-3
10. LAPC-4 CL
11. PrEC
12. HT1197
13. SCaBER
14. UM-UC-3
15. TCCSUP
16. J82
17. 5637
18. RD-ES
19. 293T
20. PANC-1
21. BxPC-3
22. HPAC
23. Capan-1
24. LS180
25. SK-CO-1
26. CaCo-2
27. LoVo
28. T84
29. Colo-205
30. BT-20
31. CAMA-1
32. DU4475
33. MCF-7
34. MDA-MB-435s
35. NTERA-2
36. NCCIT
37. TERA-1
38. TERA-2
39. A431
40. HeLa
41. OV-1063
42. PA-1
43. SW626
44. CAOV-3

FIG. 17

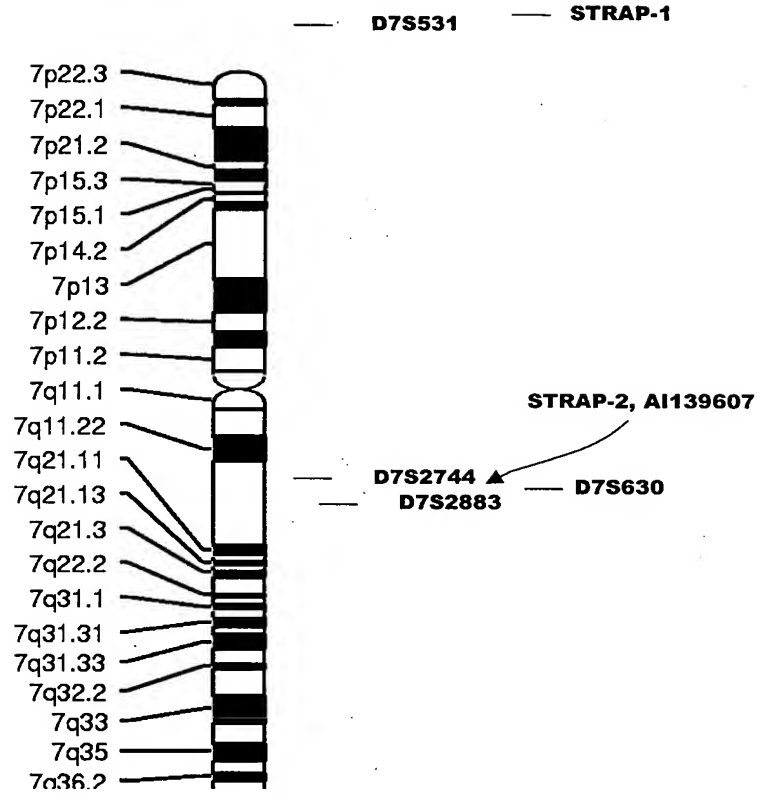


FIG. 18

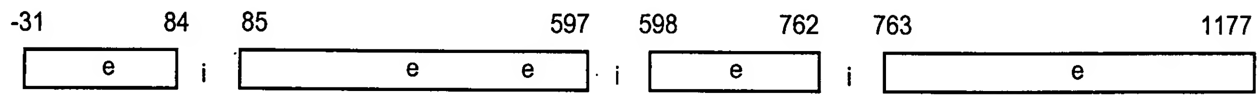


FIG. 19

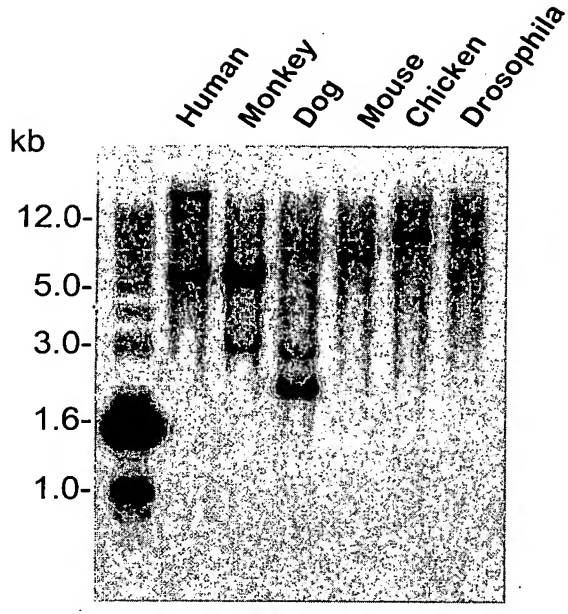
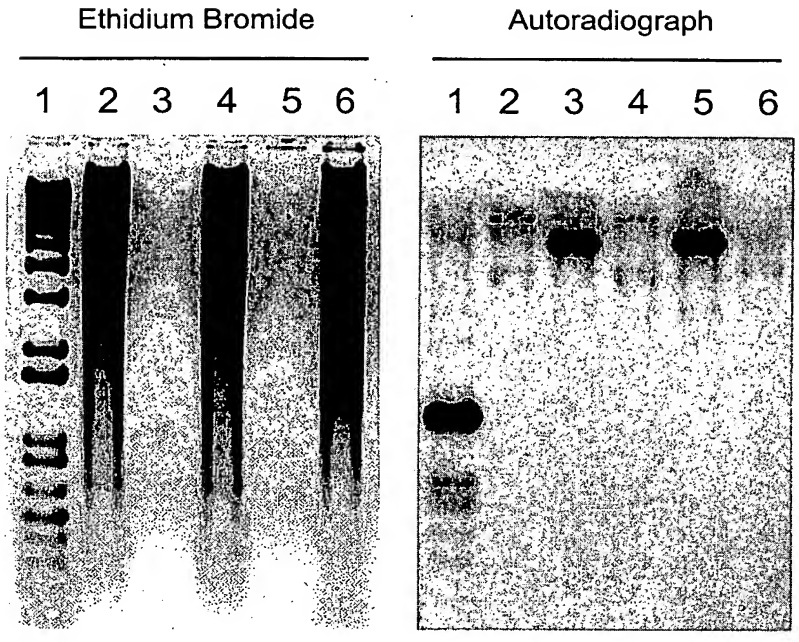


FIG. 20



Lanes

1) 1kb ladder
2) human female genomic
3) 12P11 BAC mus
4) human female genomic
5) 12P11 BAC mus
6) 3T3